

SEQUENCE LISTING

<110> ZHU, JIAN-KANG

SHI, HUAZHONG

ISHITANI, MANABU

STEVENSON, BECKY

<120> PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS

<130> 205644US20

<140> 09/824,734

<141> 2001-04-04

<150> US 60/194,648

<151> 2000-04-04

<160> 20

<170> PatentIn version 3.1

<210> 1

<211> 6076

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (226)

<223>

<220>

<221> CDS

<222> (330) .. (380)

<223>

<220>

<221> CDS

<222> (459) .. (550)

<223>

<220>

<221> CDS

<222> (631) .. (708)

<223>

<220>

<221> CDS

<222> (804) .. (961)

<223>

<220>

<221> CDS

<222> (1044)..(1145)

<223>

<220>

<221> CDS

<222> (1235)..(1352)

<223>

<220>

<221> CDS

<222> (1432)..(1484)

<223>

<220>

<221> CDS

<222> (1571)..(1636)

<223>

<220>

<221> CDS

<222> (1738)..(1782)

<223>

<220>

<221> CDS

<222> (1933)..(1985)

<223>

<220>

<221> CDS

<222> (2470) .. (2654)

<223>

<220>

<221> CDS

<222> (2767) .. (2811)

<223>

<220>

<221> CDS

<222> (2899) .. (3006)

<223>

<220>

<221> CDS

<222> (3222) .. (3453)

<223>

<220>

<221> CDS

<222> (3531) .. (3830)

<223>

<220>
<221> CDS
<222> (4012) .. (4109)
<223>

<220>
<221> CDS
<222> (4193) .. (4324)
<223>

<220>
<221> CDS
<222> (4407) .. (4625)
<223>

<220>
<221> CDS
<222> (4712) .. (4915)
<223>

<220>
<221> CDS
<222> (5003) .. (5273)
<223>

<220>

<221> CDS

<222> (5375)..(5673)

<223>

<220>

<221> CDS

<222> (5771)..(6073)

<223>

<400> 1
atg acg act gta atc gac gcg acg atg gcg tat aga ttt ctg gag gaa 48
Met Thr Thr Val Ile Asp Ala Thr Met Ala Tyr Arg Phe Leu Glu Glu
1 5 10 15
gcg acc gat tcg tct tct tct tct tct tct tcc aaa cta gaa tct agc 96
Ala Thr Asp Ser Ser Ser Ser Ser Ser Ser Lys Leu Glu Ser Ser
20 25 30
cct gtc gac gcc gtt ctc ttc gtc gga atg tct ctg gta ctc ggt att 144
Pro Val Asp Ala Val Leu Phe Val Gly Met Ser Leu Val Leu Gly Ile
35 40 45
gct tct agg cac ttg ctt cgt gga act agg gtt cct tac act gtc gct 192
Ala Ser Arg His Leu Leu Arg Gly Thr Arg Val Pro Tyr Thr Val Ala
50 55 60
ctt ctc gtt atc gga att gct ctt gga tct ctc g gttcgatttc 236
Leu Leu Val Ile Gly Ile Ala Leu Gly Ser Leu
65 70 75
gttccatgga atttctgatt tcttcatctg ttttaatcct tgaagtcaac gtaatcatgc 296
ttaattgcta attcatgttg tttggtgttt cag aa tat gga gct aaa cat aac 349
Glu Tyr Gly Ala Lys His Asn
80
ctt gga aag atc ggc cat gga att cgt atc t gtaagttttt agtttcgaat 400
Leu Gly Lys Ile Gly His Gly Ile Arg Ile
85 90
ttttcttctc ttccatggct ggctttgtaa gaactataga atcaatgtta ttgtgcag 458
gg aat gag atc gat cca gaa ctt ctt tta gct gtt ttt ctt ccg gct 505

Trp Asn Glu Ile Asp Pro Glu Leu Leu Ala Val Phe Leu Pro Ala	
95 100 105	
ctt ctt ttc gag agt tcg ttt tca atg gaa gtt cac caa att aag	550
Leu Leu Phe Glu Ser Ser Phe Ser Met Glu Val His Gln Ile Lys	
110 115 120	
gtttattcct ctggctctaa ttctagttta agcttaaagg ttaagagaaa taggtactga	610
atacttgcat gattctttag agg tgt ctg gga caa atg gtg tta ctt gct gtc	663
Arg Cys Leu Gly Gln Met Val Leu Leu Ala Val	
125 130	
cct gga gtt ctt att tca aca gct tgt ctt gga tcg ctt gtg aag	708
Pro Gly Val Leu Ile Ser Thr Ala Cys Leu Gly Ser Leu Val Lys	
135 140 145	
gtatgaatta gcctgggttg tattaagtag ctgtcctgaa aacaaagaaa gacaaatcga	768
ttattatggt atgaaactat acttgctata tgcag gtc acg ttt ccg tat gaa	821
Val Thr Phe Pro Tyr Glu	
150 155	
tgg gac tgg aaa acg tcc ttg ttg ctt ggg gga ctt tta agt gct act	869
Trp Asp Trp Lys Thr Ser Leu Leu Leu Gly Gly Leu Leu Ser Ala Thr	
160 165 170	
gat ccg gtt gct gtt gtt gct ttg cta aag gag ctt ggt gct agt aag	917
Asp Pro Val Ala Val Val Ala Leu Leu Lys Glu Leu Gly Ala Ser Lys	
175 180 185	
aag cta agc acc ata att gaa ggg gaa tcc ctg atg aat gat gg	961
Lys Leu Ser Thr Ile Ile Glu Gly Glu Ser Leu Met Asn Asp Gly	
190 195 200	
gtaaatagacg ttatcttctg tcatggtttg gttagttttg acatttatgc tcactcttca	1021
tgatttttaa caacaattcc ag g acg gcg att gtt gtt ttc cag tta ttc	1071
Thr Ala Ile Val Val Phe Gln Leu Phe	
205 210	
tta aag atg gct atg ggg caa aac tct gac tgg agt tct ata atc aaa	1119
Leu Lys Met Ala Met Gly Gln Asn Ser Asp Trp Ser Ser Ile Ile Lys	
215 220 225	
ttt ctg ctt aaa gtc gca ctt gga gc gtatgtcttg atcttttttc	1165
Phe Leu Leu Lys Val Ala Leu Gly Ala	
230 235	
atctgttggt agtgatatca agttgctgct gtgttcttat cagtccaacg tggttcttctg	1225
tctatttag t gta ggc att ggt ctg gcg ttt ggc att gca tca gtt att	1274

Val Gly Ile Gly Leu Ala Phe Gly Ile Ala Ser Val Ile
 240 245

tgg ctc aag ttc ata ttc aat gac act gta ata gag att act ctt aca 1322
 Trp Leu Lys Phe Ile Phe Asn Asp Thr Val Ile Glu Ile Thr Leu Thr
 250 255 260 265

att gca gtg agc tat ttc gca tac tac act gtacgtcttt ctgtagacct 1372
 Ile Ala Val Ser Tyr Phe Ala Tyr Tyr Thr
 270 275

tgaattcctg tgctaagata ttctctttgt agtaaaactg agagtttatt gtgtgacag 1431

gct caa gag tgg gct ggg gct tct ggt gtt ttg acg gtc atg act ttg 1479
 Ala Gln Glu Trp Ala Gly Ala Ser Gly Val Leu Thr Val Met Thr Leu
 280 285 290

ggc at gtaaatttca gtgatctcgt tatttttttt ttccctttct tttgttatca 1534
 Gly Met

tttaagaagt ctcttctcat aaaataactg taacag g ttt tat gct gca ttt gca 1589
 Phe Tyr Ala Ala Phe Ala
 295

agg aca gcc ttt aaa ggt gac agt caa aaa agc ttg cat cac ttc tg 1636
 Arg Thr Ala Phe Lys Gly Asp Ser Gln Lys Ser Leu His His Phe Trp
 300 305 310

gtatttccag aacttgtgga atttggactt gtttttttat attgtaactc tatgtaaaag 1696

gttgatctgt gtgatataaa ttttcccggt aacttgtgca g g gaa atg gtt gca 1750
 Glu Met Val Ala

tat att gca aac act ttg ata ttt atc ctc ag gtaagggtaa attttataga 1802
 Tyr Ile Ala Asn Thr Leu Ile Phe Ile Leu Ser
 320 325

ctcatatcat gcttgtgctt gccaaccta aaatagaagc tcatgggtag aaaaaagagc 1862

tattttactg cagtctactc tttagcctgg tgttgcaata ttgactgtgt ttctcgtttt 1922

atgtttgcag t ggt gtt gtc att gct gaa ggc att ctc gac agt gat aag 1972
 Gly Val Val Ile Ala Glu Gly Ile Leu Asp Ser Asp Lys
 335 340

att gcc tac caa g gtgccattat ttaatgttga tagtgtacag tatttttttc 2025
 Ile Ala Tyr Gln
 345

ctagctaaag taaattttgt gaacatagtt ttgtctgcat tttcgacagt tcaactgttaa 2085

ttgaagatga gatctaagtc attacatagg actcccacct gttatcatag ttttctgtcg	2145
ttgttaacac accttactgt tcatgggtctt tggttctcga aggatcacta attccataac	2205
gtgaatcagt tacaagaata agaaaaaac tggcattatt ggttacgaaa tattgagcga	2265
aagttaccac tgtgctagga ctgagacaat tgtattcttt caccagtctg ttattattat	2325
taagtacctg ttagagatgt actgtcttgg aaccatatat tttttctctg gaaccatatc	2385
tgcataaggc acatgatata ctttaacttta actatTTTTT atattttgga tctaacaact	2445
cttcacgacc caaatttctt acag gg aat tca tgg cga ttt ctt ttt ctg	2495
Gly Asn Ser Trp Arg Phe Leu Phe Leu	
350 355	
cta tac gtt tac atc caa cta tcg cgt gtt gtt gtt gtt gga gtt cta	2543
Leu Tyr Val Tyr Ile Gln Leu Ser Arg Val Val Val Val Gly Val Leu	
360 365 370	
tat cca ctt tta tgt cgt ttt ggc tat ggt ttg gat tgg aaa gaa tcc	2591
Tyr Pro Leu Leu Cys Arg Phe Gly Tyr Gly Leu Asp Trp Lys Glu Ser	
375 380 385	
att ata ctc gta tgg tct ggt ttg agg ggc gca gtg gct ctt gca ctt	2639
Ile Ile Leu Val Trp Ser Gly Leu Arg Gly Ala Val Ala Leu Ala Leu	
390 395 400	
tct tta tcc gtg aag gttaatttta agaacatctg ttaaagttgt tcttctctct	2694
Ser Leu Ser Val Lys	
405	
taaatttctg cacaatgttt ttttccagcc acattgattc tgtgctgact tactcgact	2754
catttgattc ag caa tca agc gga aat tca cat atc agc aag gag act gga	2805
Gln Ser Ser Gly Asn Ser His Ile Ser Lys Glu Thr Gly	
410 415 420	
aca ttg gtaagttagt ctaaagatgt tattgacaac ttaaaatgat tatgcaaatt	2861
Thr Leu	
attgttttgt ctcttcatat tctcagttct tttgcag ttt ctt ttc ttc acg ggt	2916
Phe Leu Phe Phe Thr Gly	
425 430	
gga att gtg ttc cta act ctg ata gtt aat gga tcc act acc caa ttt	2964
Gly Ile Val Phe Leu Thr Leu Ile Val Asn Gly Ser Thr Thr Gln Phe	
435 440 445	
gtt cta cgc ctt ctt cgc atg gat att tta cca gcc ccc aag	3006
Val Leu Arg Leu Leu Arg Met Asp Ile Leu Pro Ala Pro Lys	

450

455

460

gtcaaaaact tctctcatac gaataacttt ccgagtttta agtaatcaaa tatatgtgta	3066
aacagagatt tttttgctta tgctttgtat tcatgtgtaa gtgaccgtgt tagcctgagt	3126
ctgagccttt aagctgtata gttcaatagg gtctgtatgt tctagtcagt aatgtattcg	3186
aagaacctta ttagaaacca ctttcctttt gacag aaa cga ata ttg gaa tat	3239
Lys Arg Ile Leu Glu Tyr	465
aca aag tac gaa atg ttg aat aag gcc tta cga gcg ttt caa gat cta	3287
Thr Lys Tyr Glu Met Leu Asn Lys Ala Leu Arg Ala Phe Gln Asp Leu	470 475 480
gga gac gat gag gag cta gga cct gct gac tgg cct aca gtt gaa agt	3335
Gly Asp Asp Glu Glu Leu Gly Pro Ala Asp Trp Pro Thr Val Glu Ser	485 490 495
tat att tca agc cta aaa ggt tca gaa ggg gaa cta gtt cat cat cct	3383
Tyr Ile Ser Ser Leu Lys Gly Ser Glu Gly Glu Leu Val His His Pro	500 505 510
cac aat ggc tct aaa att gga agt ctt gac cct aaa agt tta aag gac	3431
His Asn Gly Ser Lys Ile Gly Ser Leu Asp Pro Lys Ser Leu Lys Asp	515 520 525 530
ata cgt atg cgg ttc tta aat g gtagttatga tcatgtaccc tccaatatac	3483
Ile Arg Met Arg Phe Leu Asn	535
tattttacct ggtagattat tgacactttg aaaattgggt gtgtcag gt gtg caa	3538
Gly Val Gln	540
gca act tac tgg gag atg ctt gat gag ggc aga ata tct gaa gtt act	3586
Ala Thr Tyr Trp Glu Met Leu Asp Glu Gly Arg Ile Ser Glu Val Thr	545 550 555
gct aat att ttg atg cag tca gtg gat gag gcg ctt gat cag gtt tct	3634
Ala Asn Ile Leu Met Gln Ser Val Asp Glu Ala Leu Asp Gln Val Ser	560 565 570
aca act tta tgt gat tgg aga ggt cta aaa cca cat gtc aat ttc cca	3682
Thr Thr Leu Cys Asp Trp Arg Gly Leu Lys Pro His Val Asn Phe Pro	575 580 585
aat tac tac aac ttt ctt cat tct aaa gtt gtc cca cgc aag ttg gtc	3730
Asn Tyr Tyr Asn Phe Leu His Ser Lys Val Val Pro Arg Lys Leu Val	590 595 600

aca tac ttt gct gtc gaa aga cta gaa tct gct tgc tac att tct gct	3778
Thr Tyr Phe Ala Val Glu Arg Leu Glu Ser Ala Cys Tyr Ile Ser Ala	
605 610 615 620	
gcg ttt ctt cgc gca cat aca att gca cga cag caa ttg tat gat ttt	3826
Ala Phe Leu Arg Ala His Thr Ile Ala Arg Gln Gln Leu Tyr Asp Phe	
625 630 635	
cta g gtatgtacaa tccatactct gcagtctgca tcacactttg aaaacaatga	3880
Leu	
ctaagaataa aacttgtacc gtatcatcat taattgtcag agtttttgggt tgcaagtatc	3940
tcaacttagt aagaacaata cattaacca accctagttt tgtctcatac ttatctatct	4000
tctctacaca g gg gag agt aat att ggt tcc att gta atc aat gaa agt	4049
Gly Glu Ser Asn Ile Gly Ser Ile Val Ile Asn Glu Ser	
640 645 650	
gaa aag gaa gga gag gaa gca aaa aag ttc ttg gaa aaa gtc cga tct	4097
Glu Lys Glu Gly Glu Glu Ala Lys Lys Phe Leu Glu Lys Val Arg Ser	
655 660 665	
tca ttt cct cag gttgagagtc ttgtcatttc tttcgggtga cttatctttc	4149
Ser Phe Pro Gln	
670	
ttgcgggtgag gcacatataa tcttttgatta acattgggttt cag gtt ctc cgt gtt	4204
Val Leu Arg Val	
gtg aaa aca aaa caa gta aca tat tca gtg ttg aat cat tta ctc ggt	4252
Val Lys Thr Lys Gln Val Thr Tyr Ser Val Leu Asn His Leu Leu Gly	
675 680 685 690	
tac att gaa aac ctc gag aag gtt ggc ttg ttg gag gaa aaa gaa atc	4300
Tyr Ile Glu Asn Leu Glu Lys Val Gly Leu Leu Glu Glu Lys Glu Ile	
695 700 705	
gct cat ctt cat gat gct gtc cag gtaccaaatt aaagaatctc attccttcaa	4354
Ala His Leu His Asp Ala Val Gln	
710	
ctatagtctt gtctcttttg tcttatgctt ttgggtcaaatt ctatctctgc ag acc ggc	4412
Thr Gly	
715	
ttg aaa aag ctt ttg aga aac cct cca ata gtt aaa ctt cca aaa ttg	4460
Leu Lys Lys Leu Leu Arg Asn Pro Pro Ile Val Lys Leu Pro Lys Leu	
720 725 730	

agc gac atg atc acc tca cat ccg tta tcg gtt gct ctt cct cct gca	4508
Ser Asp Met Ile Thr Ser His Pro Leu Ser Val Ala Leu Pro Pro Ala	
735 740 745	
ttt tgt gaa cct tta aaa cac tcg aaa aaa gaa cca atg aaa ctg cgt	4556
Phe Cys Glu Pro Leu Lys His Ser Lys Lys Glu Pro Met Lys Leu Arg	
750 755 760	
ggt gtc acg ctt tat aaa gaa ggt tca aag cca act gga gtc tgg ctt	4604
Gly Val Thr Leu Tyr Lys Glu Gly Ser Lys Pro Thr Gly Val Trp Leu	
765 770 775 780	
att ttt gat ggc atc gtt aag gtaacccaaa acttatcttt tactttttaac	4655
Ile Phe Asp Gly Ile Val Lys	
785	
tcgtaagtct gtatgatcta ttaccttcat aactgaatgt tataacaatc ctacag tgg	4714
Trp	
aaa agt aag atc tta agc aac aat cac tcg ctg cat cca act ttt tct	4762
Lys Ser Lys Ile Leu Ser Asn Asn His Ser Leu His Pro Thr Phe Ser	
790 795 800	
cac ggt agt aca ttg gga ctc tac gaa gtc ctc act ggg aag cca tat	4810
His Gly Ser Thr Leu Gly Leu Tyr Glu Val Leu Thr Gly Lys Pro Tyr	
805 810 815 820	
ctg tgc gac ttg att aca gat tct atg gtt ctt tgc ttt ttc att gat	4858
Leu Cys Asp Leu Ile Thr Asp Ser Met Val Leu Cys Phe Phe Ile Asp	
825 830 835	
agc gag aaa att cta tca cta caa tca gat tct acc atc gat gat ttc	4906
Ser Glu Lys Ile Leu Ser Leu Gln Ser Asp Ser Thr Ile Asp Asp Phe	
840 845 850	
ctt tgg cag gtacgtctct attagaatcc attttagaga gactcatttc	4955
Leu Trp Gln	
855	
ttgattgtta agttgcttca actttttttcg gtttttttttg tttgcag gaa agt gca	5011
Glu Ser Ala	
ttg gtt ctt ctc aaa ctc ttg cgt cct cag ata ttt gaa agt gtg gca	5059
Leu Val Leu Leu Lys Leu Leu Arg Pro Gln Ile Phe Glu Ser Val Ala	
860 865 870	
atg caa gaa tta cga gcc ctt gtt tca act gaa agc tcg aaa ctt aca	5107
Met Gln Glu Leu Arg Ala Leu Val Ser Thr Glu Ser Ser Lys Leu Thr	
875 880 885 890	

aca tat gtg acg gga gaa tca atc gaa atc gac tgc aac agc att ggt	5155
Thr Tyr Val Thr Gly Glu Ser Ile Glu Ile Asp Cys Asn Ser Ile Gly	
895 900 905	
tta tta tta gaa gga ttc gta aaa ccg gtt ggt atc aaa gaa gag ctt	5203
Leu Leu Leu Glu Gly Phe Val Lys Pro Val Gly Ile Lys Glu Glu Leu	
910 915 920	
ata tca tct ccc gcc gca tta tca cct tct aac ggg aat caa agc ttc	5251
Ile Ser Ser Pro Ala Ala Leu Ser Pro Ser Asn Gly Asn Gln Ser Phe	
925 930 935	
cat aat tca tca gaa gct tca g gtaattaatt gcacagtaca gcaggatcaa	5303
His Asn Ser Ser Glu Ala Ser	
940 945	
accttttttaa atgtcagcga atgatataaa tcgaattaaa tcaaaaatgt gttttgtttt	5363
tttgaccaca g gt atc atg aga gtc agt ttc tca caa caa gca aca cag	5412
Gly Ile Met Arg Val Ser Phe Ser Gln Gln Ala Thr Gln	
950 955	
tat att gtt gag acg aga gca aga gca atc atc ttc aac att gga gca	5460
Tyr Ile Val Glu Thr Arg Ala Arg Ala Ile Ile Phe Asn Ile Gly Ala	
960 965 970	
ttt gga gct gat agg act cta cat cga aga cca tct tcg tta aca cca	5508
Phe Gly Ala Asp Arg Thr Leu His Arg Arg Pro Ser Ser Leu Thr Pro	
975 980 985 990	
cca cgt agc tca agc tct gat cag ctt cag aga tca ttt cgt aaa gaa	5556
Pro Arg Ser Ser Ser Ser Asp Gln Leu Gln Arg Ser Phe Arg Lys Glu	
995 1000 1005	
cac aga ggt ctc atg agc tgg cct gaa aat att tac gcc aaa caa	5601
His Arg Gly Leu Met Ser Trp Pro Glu Asn Ile Tyr Ala Lys Gln	
1010 1015 1020	
caa caa gag atc aat aaa acg aca tta agt tta tct gaa cga gca	5646
Gln Gln Glu Ile Asn Lys Thr Thr Leu Ser Leu Ser Glu Arg Ala	
1025 1030 1035	
atg caa ctc agc att ttc ggc agc atg gtaaaaaaga tctcaatgtt	5693
Met Gln Leu Ser Ile Phe Gly Ser Met	
1040 1045	
gattctttta aagggttgta tcgatgaact tctcgactaa cctgaagggtt tttatcttct	5753
gatattctcg aatatag gtt aat gtg tac aga agg agt gta agt ttc ggt	5803
Val Asn Val Tyr Arg Arg Ser Val Ser Phe Gly	
1050 1055	

ggg	atc	tat	aat	aac	aag	tta	caa	gat	aac	ttg	ttg	tac	aaa	aaa	5848
Gly	Ile	Tyr	Asn	Asn	Lys	Leu	Gln	Asp	Asn	Leu	Leu	Tyr	Lys	Lys	
			1060					1065					1070		

ctt	cca	cta	aac	cca	gct	caa	ggt	ctc	ggt	tca	gcc	aaa	tca	gaa	5893
Leu	Pro	Leu	Asn	Pro	Ala	Gln	Gly	Leu	Val	Ser	Ala	Lys	Ser	Glu	
			1075					1080					1085		

agt	tca	att	gtg	acc	aag	aag	cag	ctt	gaa	acc	cgt	aaa	cat	gcg	5938
Ser	Ser	Ile	Val	Thr	Lys	Lys	Gln	Leu	Glu	Thr	Arg	Lys	His	Ala	
			1090					1095					1100		

tgt	cag	ctt	cct	ctg	aaa	ggg	gaa	agc	agc	aca	agg	caa	aat	acg	5983
Cys	Gln	Leu	Pro	Leu	Lys	Gly	Glu	Ser	Ser	Thr	Arg	Gln	Asn	Thr	
			1105					1110					1115		

atg	gtt	gaa	tca	agc	gat	gaa	gaa	gat	gaa	gat	gaa	gga	atc	gtt	6028
Met	Val	Glu	Ser	Ser	Asp	Glu	Glu	Asp	Glu	Asp	Glu	Gly	Ile	Val	
			1120					1125					1130		

gtg	aga	atc	gat	tct	ccg	agt	aaa	atc	gtt	ttc	agg	aac	gat	cta	6073
Val	Arg	Ile	Asp	Ser	Pro	Ser	Lys	Ile	Val	Phe	Arg	Asn	Asp	Leu	
			1135					1140					1145		

tga															6076
-----	--	--	--	--	--	--	--	--	--	--	--	--	--	--	------

<210> 2

<211> 1146

<212> PRT

<213> Arabidopsis thaliana

<400> 2

Met	Thr	Thr	Val	Ile	Asp	Ala	Thr	Met	Ala	Tyr	Arg	Phe	Leu	Glu	Glu
1				5					10					15	

Ala	Thr	Asp	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Leu	Glu	Ser	Ser
			20					25					30		

Pro	Val	Asp	Ala	Val	Leu	Phe	Val	Gly	Met	Ser	Leu	Val	Leu	Gly	Ile
		35					40					45			

Ala	Ser	Arg	His	Leu	Leu	Arg	Gly	Thr	Arg	Val	Pro	Tyr	Thr	Val	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50

55

60

Leu Leu Val Ile Gly Ile Ala Leu Gly Ser Leu Glu Tyr Gly Ala Lys
65 70 75 80

His Asn Leu Gly Lys Ile Gly His Gly Ile Arg Ile Trp Asn Glu Ile
85 90 95

Asp Pro Glu Leu Leu Leu Ala Val Phe Leu Pro Ala Leu Leu Phe Glu
100 105 110

Ser Ser Phe Ser Met Glu Val His Gln Ile Lys Arg Cys Leu Gly Gln
115 120 125

Met Val Leu Leu Ala Val Pro Gly Val Leu Ile Ser Thr Ala Cys Leu
130 135 140

Gly Ser Leu Val Lys Val Thr Phe Pro Tyr Glu Trp Asp Trp Lys Thr
145 150 155 160

Ser Leu Leu Leu Gly Gly Leu Leu Ser Ala Thr Asp Pro Val Ala Val
165 170 175

Val Ala Leu Leu Lys Glu Leu Gly Ala Ser Lys Lys Leu Ser Thr Ile
180 185 190

Ile Glu Gly Glu Ser Leu Met Asn Asp Gly Thr Ala Ile Val Val Phe
195 200 205

Gln Leu Phe Leu Lys Met Ala Met Gly Gln Asn Ser Asp Trp Ser Ser
210 215 220

Ile Ile Lys Phe Leu Leu Lys Val Ala Leu Gly Ala Val Gly Ile Gly
225 230 235 240

Leu Ala Phe Gly Ile Ala Ser Val Ile Trp Leu Lys Phe Ile Phe Asn
245 250 255

Asp Thr Val Ile Glu Ile Thr Leu Thr Ile Ala Val Ser Tyr Phe Ala

260

265

270

Tyr Tyr Thr Ala Gln Glu Trp Ala Gly Ala Ser Gly Val Leu Thr Val
 275 280 285

Met Thr Leu Gly Met Phe Tyr Ala Ala Phe Ala Arg Thr Ala Phe Lys
 290 295 300

Gly Asp Ser Gln Lys Ser Leu His His Phe Trp Glu Met Val Ala Tyr
 305 310 315 320

Ile Ala Asn Thr Leu Ile Phe Ile Leu Ser Gly Val Val Ile Ala Glu
 325 330 335

Gly Ile Leu Asp Ser Asp Lys Ile Ala Tyr Gln Gly Asn Ser Trp Arg
 340 345 350

Phe Leu Phe Leu Leu Tyr Val Tyr Ile Gln Leu Ser Arg Val Val Val
 355 360 365

Val Gly Val Leu Tyr Pro Leu Leu Cys Arg Phe Gly Tyr Gly Leu Asp
 370 375 380

Trp Lys Glu Ser Ile Ile Leu Val Trp Ser Gly Leu Arg Gly Ala Val
 385 390 395 400

Ala Leu Ala Leu Ser Leu Ser Val Lys Gln Ser Ser Gly Asn Ser His
 405 410 415

Ile Ser Lys Glu Thr Gly Thr Leu Phe Leu Phe Phe Thr Gly Gly Ile
 420 425 430

Val Phe Leu Thr Leu Ile Val Asn Gly Ser Thr Thr Gln Phe Val Leu
 435 440 445

Arg Leu Leu Arg Met Asp Ile Leu Pro Ala Pro Lys Lys Arg Ile Leu
 450 455 460

Glu Tyr Thr Lys Tyr Glu Met Leu Asn Lys Ala Leu Arg Ala Phe Gln

465

470

475

480

Asp Leu Gly Asp Asp Glu Glu Leu Gly Pro Ala Asp Trp Pro Thr Val
 485 490 495

Glu Ser Tyr Ile Ser Ser Leu Lys Gly Ser Glu Gly Glu Leu Val His
 500 505 510

His Pro His Asn Gly Ser Lys Ile Gly Ser Leu Asp Pro Lys Ser Leu
 515 520 525

Lys Asp Ile Arg Met Arg Phe Leu Asn Gly Val Gln Ala Thr Tyr Trp
 530 535 540

Glu Met Leu Asp Glu Gly Arg Ile Ser Glu Val Thr Ala Asn Ile Leu
 545 550 555 560

Met Gln Ser Val Asp Glu Ala Leu Asp Gln Val Ser Thr Thr Leu Cys
 565 570 575

Asp Trp Arg Gly Leu Lys Pro His Val Asn Phe Pro Asn Tyr Tyr Asn
 580 585 590

Phe Leu His Ser Lys Val Val Pro Arg Lys Leu Val Thr Tyr Phe Ala
 595 600 605

Val Glu Arg Leu Glu Ser Ala Cys Tyr Ile Ser Ala Ala Phe Leu Arg
 610 615 620

Ala His Thr Ile Ala Arg Gln Gln Leu Tyr Asp Phe Leu Gly Glu Ser
 625 630 635 640

Asn Ile Gly Ser Ile Val Ile Asn Glu Ser Glu Lys Glu Gly Glu Glu
 645 650 655

Ala Lys Lys Phe Leu Glu Lys Val Arg Ser Ser Phe Pro Gln Val Leu
 660 665 670

Arg Val Val Lys Thr Lys Gln Val Thr Tyr Ser Val Leu Asn His Leu

675

680

685

Leu Gly Tyr Ile Glu Asn Leu Glu Lys Val Gly Leu Leu Glu Glu Lys
690 695 700

Glu Ile Ala His Leu His Asp Ala Val Gln Thr Gly Leu Lys Lys Leu
705 710 715 720

Leu Arg Asn Pro Pro Ile Val Lys Leu Pro Lys Leu Ser Asp Met Ile
725 730 735

Thr Ser His Pro Leu Ser Val Ala Leu Pro Pro Ala Phe Cys Glu Pro
740 745 750

Leu Lys His Ser Lys Lys Glu Pro Met Lys Leu Arg Gly Val Thr Leu
755 760 765

Tyr Lys Glu Gly Ser Lys Pro Thr Gly Val Trp Leu Ile Phe Asp Gly
770 775 780

Ile Val Lys Trp Lys Ser Lys Ile Leu Ser Asn Asn His Ser Leu His
785 790 795 800

Pro Thr Phe Ser His Gly Ser Thr Leu Gly Leu Tyr Glu Val Leu Thr
805 810 815

Gly Lys Pro Tyr Leu Cys Asp Leu Ile Thr Asp Ser Met Val Leu Cys
820 825 830

Phe Phe Ile Asp Ser Glu Lys Ile Leu Ser Leu Gln Ser Asp Ser Thr
835 840 845

Ile Asp Asp Phe Leu Trp Gln Glu Ser Ala Leu Val Leu Leu Lys Leu
850 855 860

Leu Arg Pro Gln Ile Phe Glu Ser Val Ala Met Gln Glu Leu Arg Ala
865 870 875 880

Leu Val Ser Thr Glu Ser Ser Lys Leu Thr Thr Tyr Val Thr Gly Glu

885

890

895

Ser Ile Glu Ile Asp Cys Asn Ser Ile Gly Leu Leu Leu Glu Gly Phe
 900 905 910

Val Lys Pro Val Gly Ile Lys Glu Glu Leu Ile Ser Ser Pro Ala Ala
 915 920 925

Leu Ser Pro Ser Asn Gly Asn Gln Ser Phe His Asn Ser Ser Glu Ala
 930 935 940

Ser Gly Ile Met Arg Val Ser Phe Ser Gln Gln Ala Thr Gln Tyr Ile
 945 950 955 960

Val Glu Thr Arg Ala Arg Ala Ile Ile Phe Asn Ile Gly Ala Phe Gly
 965 970 975

Ala Asp Arg Thr Leu His Arg Arg Pro Ser Ser Leu Thr Pro Pro Arg
 980 985 990

Ser Ser Ser Ser Asp Gln Leu Gln Arg Ser Phe Arg Lys Glu His Arg
 995 1000 1005

Gly Leu Met Ser Trp Pro Glu Asn Ile Tyr Ala Lys Gln Gln Gln
 1010 1015 1020

Glu Ile Asn Lys Thr Thr Leu Ser Leu Ser Glu Arg Ala Met Gln
 1025 1030 1035

Leu Ser Ile Phe Gly Ser Met Val Asn Val Tyr Arg Arg Ser Val
 1040 1045 1050

Ser Phe Gly Gly Ile Tyr Asn Asn Lys Leu Gln Asp Asn Leu Leu
 1055 1060 1065

Tyr Lys Lys Leu Pro Leu Asn Pro Ala Gln Gly Leu Val Ser Ala
 1070 1075 1080

Lys Ser Glu Ser Ser Ile Val Thr Lys Lys Gln Leu Glu Thr Arg

1085

1090

1095

Lys His Ala Cys Gln Leu Pro Leu Lys Gly Glu Ser Ser Thr Arg
 1100 1105 1110

Gln Asn Thr Met Val Glu Ser Ser Asp Glu Glu Asp Glu Asp Glu
 1115 1120 1125

Gly Ile Val Val Arg Ile Asp Ser Pro Ser Lys Ile Val Phe Arg
 1130 1135 1140

Asn Asp Leu
 1145

<210> 3

<211> 822

<212> PRT

<213> Cricetulus griseus

<400> 3

Met Met Leu Arg Trp Ser Gly Ile Trp Gly Leu Ser Pro Pro Arg Ile
 1 5 10 15

Phe Pro Ser Leu Leu Val Val Val Ala Leu Val Gly Leu Leu Pro Val
 20 25 30

Leu Arg Ser His Gly Leu Gln Pro Ser Pro Thr Ala Asn Thr Ile Arg
 35 40 45

Gly Ala Glu Pro Pro Arg Glu Arg Ser Ile Gly Asp Val Thr Thr Ala
 50 55 60

Pro Ser Glu Pro Val His His Pro Asp Asp Arg Asn Leu Thr Asn Leu
 65 70 75 80

His Ile Glu His Gly Ala Lys Thr Leu Arg Lys Ala Phe Pro Val Leu

85

90

95

Asp Ile Asp Tyr Leu His Val Arg Thr Pro Phe Glu Ile Ser Leu Trp
 100 105 110

Ile Leu Leu Ala Cys Leu Met Lys Ile Gly Phe His Val Ile Pro Thr
 115 120 125

Ile Ser Ser Ile Val Pro Glu Ser Cys Leu Leu Ile Val Val Gly Leu
 130 135 140

Leu Val Gly Gly Leu Ile Lys Gly Val Gly Glu Thr Pro Pro Phe Leu
 145 150 155 160

Gln Ser Asp Val Phe Phe Leu Phe Leu Leu Pro Pro Ile Ile Leu Asp
 165 170 175

Ala Gly Tyr Phe Leu Pro Leu Arg Gln Phe Thr Glu Asn Leu Gly Thr
 180 185 190

Ile Leu Ile Phe Ala Val Val Gly Thr Leu Trp Asn Ala Phe Phe Leu
 195 200 205

Gly Gly Leu Leu Tyr Ala Val Cys Leu Val Gly Gly Glu Gln Ile Asn
 210 215 220

Asn Ile Gly Leu Leu Asp Thr Leu Leu Phe Gly Ser Ile Ile Ser Ala
 225 230 235 240

Val Asp Pro Val Ala Val Val Ala Val Phe Glu Glu Ile His Ile Asn
 245 250 255

Glu Leu Leu His Ile Leu Val Phe Gly Glu Ser Leu Leu Asn Asp Ala
 260 265 270

Val Thr Val Val Leu Tyr His Leu Phe Glu Glu Phe Ala Asn Tyr Asp
 275 280 285

Ser Ile Gly Ile Ser Asp Ile Phe Leu Gly Phe Leu Ser Phe Phe Val

290

295

300

Val Ala Leu Gly Gly Val Phe Val Gly Val Val Tyr Gly Val Ile Ala
305 310 315 320

Ala Phe Thr Ser Arg Phe Thr Ser His Ile Arg Val Ile Glu Pro Leu
325 330 335

Phe Val Phe Leu Tyr Ser Tyr Met Ala Tyr Leu Ser Ala Glu Leu Phe
340 345 350

His Leu Ser Gly Ile Met Ala Leu Ile Ala Ser Gly Val Val Met Arg
355 360 365

Pro Tyr Val Glu Ala Asn Ile Ser His Lys Ser His Thr Thr Ile Lys
370 375 380

Tyr Phe Leu Lys Met Trp Ser Ser Val Ser Glu Thr Leu Ile Phe Ile
385 390 395 400

Phe Leu Gly Val Ser Thr Val Ala Gly Ser His Gln Trp Asn Trp Thr
405 410 415

Phe Val Ile Ser Thr Leu Leu Phe Cys Leu Ile Ala Arg Val Leu Gly
420 425 430

Val Leu Val Leu Thr Trp Phe Ile Asn Lys Phe Arg Ile Val Lys Leu
435 440 445

Thr Pro Lys Asp Gln Phe Ile Ile Ala Tyr Gly Gly Leu Arg Gly Ala
450 455 460

Ile Ala Phe Ser Leu Gly Tyr Leu Met Asp Lys Lys His Phe Pro Met
465 470 475 480

Cys Asp Leu Phe Leu Thr Ala Ile Ile Thr Val Ile Phe Phe Thr Val
485 490 495

Phe Val Gln Gly Met Thr Ile Arg Pro Leu Val Asp Leu Leu Ala Val

500

505

510

Lys Lys Lys Gln Glu Thr Lys Arg Ser Ile Asn Glu Glu Ile His Thr
515 520 525

Gln Phe Leu Asp His Leu Leu Thr Gly Ile Glu Asp Ile Cys Gly His
530 535 540

Tyr Gly His His His Trp Lys Asp Lys Leu Asn Arg Phe Asn Lys Lys
545 550 555 560

Tyr Val Lys Lys Cys Leu Ile Ala Gly Glu Arg Ser Lys Glu Pro Gln
565 570 575

Leu Ile Ala Phe Tyr His Lys Met Glu Met Lys Gln Ala Ile Glu Leu
580 585 590

Val Glu Ser Gly Gly Met Gly Lys Ile Pro Ser Ala Val Ser Thr Val
595 600 605

Ser Met Gln Asn Ile His Pro Lys Ser Met Ala Ser Glu Arg Ile Leu
610 615 620

Pro Ala Leu Ser Lys Asp Lys Glu Glu Glu Ile Arg Lys Ile Leu Arg
625 630 635 640

Ser Asn Leu Gln Lys Thr Arg Gln Arg Leu Arg Ser Tyr Asn Arg His
645 650 655

Thr Leu Val Ala Asp Pro Tyr Glu Glu Ala Trp Asn Gln Met Leu Leu
660 665 670

Arg Arg Gln Lys Ala Arg Gln Leu Glu Gln Lys Met Ser Asn Tyr Leu
675 680 685

Thr Val Pro Ala His Lys Leu Asp Ser Pro Thr Met Ser Arg Ala Arg
690 695 700

Ile Gly Ser Asp Pro Leu Ala Tyr Glu Pro Lys Ala Asp Leu Pro Val

35

40

45

Gly Tyr Pro Ile Leu Glu Val Glu Met Gln Glu Ile Ile Arg Arg Ile
50 55 60

Asp Phe Ser Glu Val Leu Met Thr Trp Phe Leu Pro Ala Leu Leu Phe
65 70 75 80

Ala Gly Ala Leu His Val Asp Leu Ser Asp Leu Arg Ser Tyr Lys Trp
85 90 95

Pro Ile Gly Leu Leu Ala Thr Ala Gly Val Leu Ile Ala Thr Phe Val
100 105 110

Ile Gly Gly Leu Ala Tyr Tyr Thr Phe Pro Leu Phe Gly Trp Gln Val
115 120 125

Asp Phe Ile Tyr Cys Leu Leu Phe Gly Ala Leu Ile Ser Pro Thr Asp
130 135 140

Pro Ile Ala Val Leu Gly Ile Leu Lys Ser Ala Gly Ala Pro Lys Pro
145 150 155 160

Leu Ala Thr Thr Ile Val Gly Glu Ser Leu Phe Asn Asp Gly Thr Ala
165 170 175

Val Val Val Phe Ala Ile Ile Leu Gly Ile Leu Gln Leu Gly Glu Ala
180 185 190

Pro Thr Val Ser Ala Thr Ala Ile Leu Phe Val Gln Glu Ala Ile Gly
195 200 205

Gly Val Val Phe Gly Ala Val Leu Gly Tyr Gly Val Phe Val Met Met
210 215 220

Arg Gly Ile Asp Gln Tyr Gln Val Glu Val Met Leu Thr Leu Ala Leu
225 230 235 240

Val Ile Gly Gly Ala Ala Leu Ala Ala Arg Leu His Val Ser Ala Pro

245

250

255

Ile Ala Met Val Val Ala Gly Leu Ile Ile Gly Asn His Gly Arg His
260 265 270

Tyr Ala Met Ser Asp Glu Thr Arg Arg Tyr Val Asp Lys Phe Trp Glu
275 280 285

Leu Ile Asp Glu Ile Leu Asn Ala Leu Leu Phe Ala Leu Ile Gly Leu
290 295 300

Glu Leu Leu Leu Leu Pro Phe Ser Trp Leu His Val Ala Ala Ala Phe
305 310 315 320

Ala Leu Gly Gly Ala Val Leu Val Ser Arg Leu Leu Thr Val Gly Pro
325 330 335

Ala Ile Leu Val Leu Arg Arg Phe Arg Gly Ala Asn Arg Gln Val Pro
340 345 350

Ala Gly Thr Ile Arg Ile Leu Val Trp Gly Gly Leu Arg Gly Gly Val
355 360 365

Ser Val Ala Leu Ala Leu Ser Leu Pro Leu Gly Pro Glu Arg Asp Leu
370 375 380

Ile Leu Ser Leu Thr Tyr Ile Val Val Leu Val Ser Ile Leu Leu Gln
385 390 395 400

Gly Leu Ser Ile Gly Pro Leu Val Arg Arg Ile Tyr Ala Gly Gln Pro
405 410 415

Leu Glu Lys Ser Glu Gly Ala His
420

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 5
ggatgatgat cgattcggat

20

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 6
atctgactca taggatatcg

20

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 7
ccttcacatc caaaacccac

20

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 8

gcacataccc acaaccagaa

20

<210> 9

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 9

gaatgttttg aaggatatct cag

23

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 10

gaaaaatgga gcacgaaatg c

21

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 11

cccagatta atacacaatc

20

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 12

gcagattatg taattgtgac c

21

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 13

tcgtgtttac cgggtcggat

20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 14
tgatgagaat cttagcgagc

20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 15
tggttaagacc aaattacact c

21

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 16
cgtaattaaa atgtgttaaa ccg

23

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 17
aaccgcatag tacaatgcag

20

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 18
cggtaaagat caactaataa cg

22

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 19

aacggaaacg gcaactagac

20

<210> 20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 20

accctaaatg tttcgattcg

20